

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Nucleotide sequences which code for the ilvE gene

<130> 000759 BT

<140>

10 <141>

<160> 2

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 1453

<212> DNA

<213> Corynebacterium glutamicum

20

<220>

<221> CDS

<222> (221) .. (1321)

<223> ilvE gene

25

<400> 1

```

ccttggttgg tgctgttgctg ctgtaggcat ttttcgccat tgaaagctga gtcctctcgt 60
tgaagttgtg tctccgcttt ggttggggga ggcatacaat tgaaactaac ttttaacaag 120
cctagccatt cctcaaaacc gtgagacgaa attggctatt catcccataa aatgggggctg 180
actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 235
Met Thr Ser Leu Glu
1 5
ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 283
Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys
10 15 20
gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 331
Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met
25 30 35
gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 379
Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu
40 45 50
gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 427
Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His
55 60 65
tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 475
Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp
70 75 80 85
gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 523
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln
90 95 100

```

	cgt	tca	gca	gct	cga	atg	gca	atg	cca	cag	ttg	cca	acc	gag	gac	ttt	571
	Arg	Ser	Ala	Ala	Arg	Met	Ala	Met	Pro	Gln	Leu	Pro	Thr	Glu	Asp	Phe	
				105					110					115			
5	att	aaa	gca	ctt	gaa	ctg	ctg	gta	gac	gcg	gat	cag	gat	tgg	gtt	cct	619
	Ile	Lys	Ala	Leu	Glu	Leu	Leu	Val	Asp	Ala	Asp	Gln	Asp	Trp	Val	Pro	
			120					125					130				
10	gag	tac	ggc	gga	gaa	gct	tcc	ctc	tac	ctg	cgc	cca	ttc	atg	atc	tcc	667
	Glu	Tyr	Gly	Gly	Glu	Ala	Ser	Leu	Tyr	Leu	Arg	Pro	Phe	Met	Ile	Ser	
			135				140					145					
15	acc	gaa	att	ggc	ttg	ggg	gtc	agc	cca	gct	gat	gcc	tac	aag	ttc	ctg	715
	Thr	Glu	Ile	Gly	Leu	Gly	Val	Ser	Pro	Ala	Asp	Ala	Tyr	Lys	Phe	Leu	
	150					155					160					165	
20	gtc	atc	gca	tcc	cca	gtc	ggc	gct	tac	ttc	acc	ggg	gga	atc	aag	cct	763
	Val	Ile	Ala	Ser	Pro	Val	Gly	Ala	Tyr	Phe	Thr	Gly	Gly	Ile	Lys	Pro	
					170					175					180		
25	gtt	tcc	gtc	tgg	ctg	agc	gaa	gat	tac	gtc	cgc	gct	gca	ccc	ggc	gga	811
	Val	Ser	Val	Trp	Leu	Ser	Glu	Asp	Tyr	Val	Arg	Ala	Ala	Pro	Gly	Gly	
				185					190					195			
30	act	ggg	gac	gcc	aaa	ttt	gct	ggc	aac	tac	gcg	gct	tct	ttg	ctt	gcc	859
	Thr	Gly	Asp	Ala	Lys	Phe	Ala	Gly	Asn	Tyr	Ala	Ala	Ser	Leu	Leu	Ala	
			200				205						210				
35	cag	tcc	cag	gct	gcg	gaa	aag	ggc	tgt	gac	cag	gtc	gta	tgg	ttg	gat	907
	Gln	Ser	Gln	Ala	Ala	Glu	Lys	Gly	Cys	Asp	Gln	Val	Val	Trp	Leu	Asp	
			215				220					225					
40	gcc	atc	gag	cac	aag	tac	atc	gaa	gaa	atg	ggg	ggc	atg	aac	ctt	ggg	955
	Ala	Ile	Glu	His	Lys	Tyr	Ile	Glu	Glu	Met	Gly	Gly	Met	Asn	Leu	Gly	
	230					235					240					245	
45	ttc	atc	tac	cgc	aac	ggc	gac	caa	gtc	aag	cta	gtc	acc	cct	gaa	ctt	1003
	Phe	Ile	Tyr	Arg	Asn	Gly	Asp	Gln	Val	Lys	Leu	Val	Thr	Pro	Glu	Leu	
					250					255					260		
50	tcc	ggc	tca	cta	ctt	cca	ggc	atc	acc	cgc	aag	tca	ctt	cta	caa	gta	1051
	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Ile	Thr	Arg	Lys	Ser	Leu	Leu	Gln	Val	
				265					270					275			
55	gca	cgc	gac	ttg	gga	tac	gaa	gta	gaa	gag	cga	aag	atc	acc	acc	acc	1099
	Ala	Arg	Asp	Leu	Gly	Tyr	Glu	Val	Glu	Glu	Arg	Lys	Ile	Thr	Thr	Thr	
			280				285						290				
60	gag	tgg	gaa	gaa	gac	gca	aag	tct	ggc	gcc	atg	acc	gag	gca	ttt		

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac 1291
 Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

5 caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga 1341
 Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

10 ccccgctgca ttaaaccctg atttattgca gcggggtttt tgcgttgaca agctcttatg 1401
 agacgtaggg ggtggaagca ggggtaggac gtgtccagcc caagtggcat gc 1453

15 <210> 2
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

20 <400> 2
 Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
 1 5 10 15

25 Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

30 His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

35 Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

40 Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

45 Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

50 Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

55 Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

	Ala	Ser	Leu	Leu	Ala	Gln	Ser	Gln	Ala	Ala	Glu	Lys	Gly	Cys	Asp	Gln
	210						215					220				
5	Val	Val	Trp	Leu	Asp	Ala	Ile	Glu	His	Lys	Tyr	Ile	Glu	Glu	Met	Gly
	225					230					235					240
	Gly	Met	Asn	Leu	Gly	Phe	Ile	Tyr	Arg	Asn	Gly	Asp	Gln	Val	Lys	Leu
					245					250					255	
10	Val	Thr	Pro	Glu	Leu	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Ile	Thr	Arg	Lys
				260					265						270	
	Ser	Leu	Leu	Gln	Val	Ala	Arg	Asp	Leu	Gly	Tyr	Glu	Val	Glu	Glu	Arg
				275				280					285			
15	Lys	Ile	Thr	Thr	Thr	Glu	Trp	Glu	Glu	Asp	Ala	Lys	Ser	Gly	Ala	Met
		290					295					300				
	Thr	Glu	Ala	Phe	Ala	Cys	Gly	Thr	Ala	Ala	Val	Ile	Thr	Pro	Val	Gly
20	305					310					315					320
	Thr	Val	Lys	Ser	Ala	His	Gly	Thr	Phe	Glu	Val	Asn	Asn	Asn	Glu	Val
					325					330					335	
25	Gly	Glu	Ile	Thr	Met	Lys	Leu	Arg	Glu	Thr	Leu	Thr	Gly	Ile	Gln	Gln
				340					345					350		
	Gly	Asn	Val	Glu	Asp	Gln	Asn	Gly	Trp	Leu	Tyr	Pro	Leu	Val	Gly	
			355					360					365			
30																